## AMENDMENTS TO THE SPECIFICATION

Kindly amend the paragraph starting at page 24, line 7, as follows.

Hippocampal brain tissue was obtained from the Harvard Brain Tissue Resource Center ~~(http://www.brainbank.mclean.org:8080/)~~ from patients with bipolar disorder (n=9), schizophrenic patients (n=8), and control patients free of mental illness (Table 1). The diagnosis of each patient was verified by two psychiatrists who reviewed the donors' medical records.

Kindly amend the paragraph starting at page 26, line 1, as follows.

The MAPPfinder program ~~(http://www.genmapp.org)~~ identifies regulatory trends among groups of genes that are organized by biological process, molecular function, or cellular component, as defined by the Gene Ontology (GO) consortium ~~(http://www.geneontology.org)~~. For algorithm verification, data were also computed with the Affymetrix Data Mining Tool (version 3.0).

Kindly amend the paragraph starting at page 44, line 18, as follows.

For Q-rt-PCR, cDNA was synthesized from 1 μg of total RNA with the Invitrogen SuperScript First-Strand Synthesis System for Q-rt-PCR (Invitrogen, CA), using Oligo dT as the Primer. A primer set for each gene was designed with the help of *Primer3* ~~(www-genome.wi.mit.edu/cgi-bin/primer/primer3.cgi)~~. Amplicons were designed to be between

100 and 150 base pairs in length. Melt curve analysis and polyacrylamide gel electrophoresis were used to confirm the specificity of each primer pair. The real-time QQ-rt-PCR reaction was performed in the MJ RESEARCH DNA ENGINE OPTICON (MJ Research, Waltham, MA; Opticon Monitor Data Analysis Software v 1.4), with the DyNAmo SYBR Green Q-rt-PCR Kit (Finnzymes, Finland), according to the company protocol, in 25 µl volume, with 2.5 µl of 1:5 diluted cDNA samples and 0.3 µM Primers. PCR cycling conditions were as follows: initially, samples were heated at 95°C for 10 minutes, followed by 49 cycles of 94°C for 30 seconds, 55°C for 30 seconds, 72°C for 30 seconds. Data were collected between 72°C and 79°C, depending on amplicon melting temperature. A melt curve analysis was performed at the end of each Q-rt-PCR experiment. Dilution curves were generated for each primer in every experiment by diluting cDNA from a control sample 1:3 twice, yielding a dilution series of 1.00, 0.333, and 0.111. The log of the dilution value was plotted against the cycle threshold (CT) value. Blanks were run with each dilution curve to control for cross contamination. Dilution curves, blanks, and samples were run in duplicate. Reported values were normalized to the internal control Human Filamin A alpha (accession # NM_001456), an actin binding protein. Filamin A alpha was not regulated in the gene array analysis or in the Q-rt-PCR analysis. Seven control samples and six bipolar disorder samples, available from the original group, were used for Q-rt-PCR.